

EXHIBIT "C"

>IPI00044749.2 ACCESSION: IPI00044749 NID: Homo sapiens (Human).
 SERINE/THREONINE-PROTEIN KINASE NEK1. IPI_human
 Length = 1258

Score = 2184 bits (5659), Expect = 0.0
 Identities = 1123/1258 (89%), Positives = 1123/1258 (89%), Gaps = 44/1258 (3%)

Query: 1 MEKYVRLQKIGEGSGFGKAILVKSTEDGRQYVIKEINIXXXXXXXXXXXXXAVLANMKH 60
 MEKYVRLQKIGEGSGFGKAILVKSTEDGRQYVIKEINI VAVLANMKH
 Sbjct: 1 MEKYVRLQKIGEGSGFGKAILVKSTEDGRQYVIKEINISRMSSKEREESRREAVLANMKH 60

Query: 61 PNIVQYRESFEENGSLYIVMDYCEGGDLFKRINAQKGVLQEDQILLDWFVQICLALKHVH 120
 PNIVQYRESFEENGSLYIVMDYCEGGDLFKRINAQKGVLQEDQILLDWFVQICLALKHVH
 Sbjct: 61 PNIVQYRESFEENGSLYIVMDYCEGGDLFKRINAQKGVLQEDQILLDWFVQICLALKHVH 120

Query: 121 DRKILHRDIKSQNIFLTKDGTVQLGDFGIARVLNSTVELARTCIGTPYYLSPEICENKPY 180
 DRKILHRDIKSQNIFLTKDGTVQLGDFGIARVLNSTVELARTCIGTPYYLSPEICENKPY
 Sbjct: 121 DRKILHRDIKSQNIFLTKDGTVQLGDFGIARVLNSTVELARTCIGTPYYLSPEICENKPY 180

Query: 181 NNKSDIWAALGCVLYELCTLKHAFEAGSMKNLVLKIISGSFPPVSLHYSYDLRSLVSQLFK 240
 NNKSDIWAALGCVLYELCTLKHAFEAGSMKNLVLKIISGSFPPVSLHYSYDLRSLVSQLFK
 Sbjct: 181 NNKSDIWAALGCVLYELCTLKHAFEAGSMKNLVLKIISGSFPPVSLHYSYDLRSLVSQLFK 240

Query: 241 RNPRDRPSVNSILEKGFIAKRIEKFLSPQLIAEEFCLKTFSKFGSQPIAKRPASGQNSI 300
 RNPRDRPSVNSILEKGFIAKRIEKFLSPQLIAEEFCLKTFSKFGSQPIAKRPASGQNSI
 Sbjct: 241 RNPRDRPSVNSILEKGFIAKRIEKFLSPQLIAEEFCLKTFSKFGSQPIAKRPASGQNSI 300

Query: 301 SVMPAQKITKPAAKYGIPLAYKKYGDKKLHEKKPLQHKQAHQTPEKRVNTGEERRKISE 360
 SVMPAQKITKPAAKYGIPLAYKKYGDKKLHEKKPLQHKQAHQTPEKRVNTGEERRKISE
 Sbjct: 301 SVMPAQKITKPAAKYGIPLAYKKYGDKKLHEKKPLQHKQAHQTPEKRVNTGEERRKISE 360

Query: 361 EAARKRRLEFXXXXXXXXXXXXSLMKAEQMKRQEKERLERINRAREQGWRNVLSAGGSGE 420
 EAARKRRLEF SLMKAEQMKRQEKERLERINRAREQGWRNVLSAGGSGE
 Sbjct: 361 EAARKRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQGWRNVLSAGGSGE 420

Query: 421 VKAPFLGSGGTIAPSSFSSRGQYEHYHAI FDQMQQQRAEDNEAKWKREIYGRGLPE--- 476
 VKAPFLGSGGTIAPSSFSSRGQYEHYHAI FDQMQQQRAEDNEAKWKREIYGRGLPE
 Sbjct: 421 VKAPFLGSGGTIAPSSFSSRGQYEHYHAI FDQMQQQRAEDNEAKWKREIYGRGLPERGIL 480

Query: 477 -----RQKGQLAVERAKQVEEFLQR 496
 RQKGQLAVERAKQVEEFLQR
 Sbjct: 481 PGVRPGFPYGAAGHHHPDADDIRKTLKRLKAVSKQANANRQKGQLAVERAKQVEEFLQR 540

Query: 497 KREAMQNKARAEGHMVYLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM 556
 KREAMQNKARAEGHMVYLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM
 Sbjct: 541 KREAMQNKARAEGHMVYLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM 600

Query: 557 RRKKIESLKAHANARAAVLKEQLXXXXXXXXXXXXVWEEHLVAKGVKSSDVSPPLGQHE 616
 RRKKIESLKAHANARAAVLKEQL VWEELVAKGVKSSDVSPPLGQHE
 Sbjct: 601 RRKKIESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLVAKGVKSSDVSPPLGQHE 660

Query: 617 TGGSPSKQQMRSVISVTSALKEVGVDSSLTDRETSEEMQKTNNAISSKREILRRLNENL 676
 TGGSPSKQQMRSVISVTSALKEVGVDSSLTDRETSEEMQKTNNAISSKREILRRLNENL
 Sbjct: 661 TGGSPSKQQMRSVISVTSALKEVGVDSSLTDRETSEEMQKTNNAISSKREILRRLNENL 720

Query: 677 KAQEDEKGMQNLSDTFeINVHEDAKEHEKEKSVDKWEAGGQLVIPLDLTLDTFS 736
 KAQEDEKG QNLSDTFeINVHEDAKEHEKEKSVDKWEAGGQLVIPLDLTLDTFS
 Sbjct: 721 KAQEDEKGKQNLSDTFeINVHEDAKEHEKEKSVDKWEAGGQLVIPLDLTLDTFS 780

Query: 737 TTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGXXXXXXXXXXXXIRSEISPEG 796
TTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILG IRSEISPEG
Sbjct: 781 TTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAELQLQTELLENTTIRSEISPEG 840

Query: 797 EKYKPLITGEKKVQCISHEINPSAIVDSPVETKSPEFSEASPQMSLKLEGNLLEPDDLET 856
EKYKPLITGEKKVQCISHEINPSAIVDSPVETKSPEFSEASPQMSLKLEGNLLEPDDLET
Sbjct: 841 EKYKPLITGEKKVQCISHEINPSAIVDSPVETKSPEFSEASPQMSLKLEGNLLEPDDLET 900

Query: 857 EILQEPSTGNKDESLPCTITDWISEEKETKETQSADRITIQCENEVSEDGVSVTVDQLSD 916
EILQEPSTGNKDESLPCTITDWISEEKETKETQSADRITIQCENEVSEDGVSVTVDQLSD
Sbjct: 901 EILQEPSTGNKDESLPCTITDWISEEKETKETQSADRITIQCENEVSEDGVSVTVDQLSD 960

Query: 917 IHIEPGTNDSQHSKCDVDKSVQPEPFFHKVVHSEHNLVPQVQSVQCSPEESFAFRSHSH 976
IHIEPGTNDSQHSKCDVDKSVQPEPFFHKVVHSEHNLVPQVQSVQCSPEESFAFRSHSH
Sbjct: 961 IHIEPGTNDSQHSKCDVDKSVQPEPFFHKVVHSEHNLVPQVQSVQCSPEESFAFRSHSH 1020

Query: 977 LPPKNNKNNSLLIGLSTGLFDANNPKMLRTCSLPDL SKLFR TLMDVPTVGDVRQXXXXXX 1036
LPPKNNKNNSLLIGLSTGLFDANNPKMLRTCSLPDL SKLFR TLMDVPTVGDVRQ
Sbjct: 1021 LPPKNNKNNSLLIGLSTGLFDANNPKMLRTCSLPDL SKLFR TLMDVPTVGDVRQDNLEID 1080

Query: 1037 XXXXXXXXGPSDSE DIVFEETDTDLQELQASMEQLLREQPGXXXXXXVLKNSDVEP 1096
GPSDSE DIVFEETDTDLQELQASMEQLLREQPG VLKNSDVEP
Sbjct: 1081 EIEDENIKEGPSDSE DIVFEETDTDLQELQASMEQLLREQPGEEYSEEESVLKNSDVEP 1140

Query: 1097 TANGTDVADEDNPSSSESALNEEWSNDGEIASECECDSVFNXXXXXXXXXXMGFE 1156
TANGTDVADEDNPSSSESALNEEWSNDGEIASECECDSVFN MGFE
Sbjct: 1141 TANGTDVADEDNPSSSESALNEEWSNDGEIASECECDSVFNHLLEELRLHLEQEMGFE 1200

Query: 1157 KFFEVYEKIKAIHEDEDENIEICSKIVQNILGNEHQHLYAKILHLMADGAYQEDNDE 1214
KFFEVYEKIKAIHEDEDENIEICSKIVQNILGNEHQHLYAKILHLMADGAYQEDNDE
Sbjct: 1201 KFFEVYEKIKAIHEDEDENIEICSKIVQNILGNEHQHLYAKILHLMADGAYQEDNDE 1258